

The applicants note, however, that preparation of corrected drawings should not be required until formal drawings are due, i.e., after allowance. The Examiner is respectfully requested to see Rule 85(c) which encourages applicants to file corrected drawings "as soon as possible following the receipt of the Notice of Allowability" as well as indicating that corrected drawings are required to be submitted at the time of allowance. Moreover, the back side of the Draftspersons Notice indicates formal drawings are not due until after receipt of the Notice of Allowability. Accordingly, applicants respectfully submit that corrected drawings should not be required in reply to Paper No. 6. The Examiner is invited to contact the undersigned, however, if anything further is required at this time in this regard or if the undersigned has overlooked some section or provision of the Law, Rules or MPEP which require submission of the formal drawings or proposed revisions to the drawings prior to an indication of allowance.

The Section 112, second paragraph, rejection of claims 49-51, 53 and 55-56 is obviated by the above amendments. Withdrawal of the Section 112, second paragraph rejection is requested.

The Section 112, first paragraph, rejection of claims 49-51, 53 and 55-56 traversed. Reconsideration and withdrawal of the rejection are requested in view of the following comments as well as the attached.

The Examiner has rejected claims 49-51, 53 and 55-56, as being drawn to prophylactic vaccine compositions, stating that a prophylactic vaccines must provide immunity, demonstrable by viral challenge experiments, in a reasonable model system. See, page 3 of Paper No. 6.

The Examiner alleges that the specification does not set forth that the claimed composition provides any sort of protective immunity in any model system that can be extrapolated to higher mammals.

In particular, the Examiner refers to Farci et al., 1997, with the comment that Farci reports that

-HCV vaccines do not exist, and

-if they exist then they would be non-efficacious, due to high reinfection rates.

The Examiner concludes that, due to

(1) the lack of success in the art,

(2) lack of working examples, and

(3) unpredictability of the generation of protective immunity, the specification is not enabling for such vaccines.

With regard to Farci et al. (1997) it is important to note that Farci's presuppositions are the following:

-the most effective clearance mechanism enacted by the immune system against viral infections would be the generation of neutralizing antibodies (page 15), and

-HVR1 is a critical neutralization domain of HCV, which would be essential for the development of an effective vaccine (p16; and Farci et al, 1996).

Even if these presuppositions would be correct, then several studies, including one of Farci et al., demonstrate that HCV can be cleared from an host, in which at least humoral mechanisms are involved, e.g., Farci et al. (Proc. Natl. Acad. Sci. USA 93: 15394-15399 (1996), copy attached) state that anti-HVR1 antiserum induced protection against homologous HCV infection in chimpanzees. Moreover, HVR1 can elicit protective immunity. This study provides direct evidence that anti-HVR1 antibodies can, in the absence of other virus-specific immune responses, prevent HCV infection. (Farci et al, 1996) Moreover, Choo et al. (1994, Proc. Natl. Acad. Sci. USA 91: 1294-1298, copy attached) demonstrate that after vaccination of 7

chimpanzees with an E1E2 fusion protein, 5 chimpanzees did not become viremic after challenge. The remaining 2 chimpanzees that became infected, showed a delayed and lower viremia and the clinical course was milder, compared to the control animals. (Choo et al. 1994). Finally, Rosa et al. (1996, Proc. Natl. Acad. Sci. USA 93: 1759-1763, copy attached) have developed a quantitative test for estimating HCV neutralizing antibodies (NOB). This test showed that there is a direct correlation between NOB antibody titers and protection from infection in vaccinated chimpanzees. (Rosa et al. 1996).

Thus, vaccination can be effective (in a limited number of cases), even based on a humoral response.

HVR1 might be an important neutralization domain, to which a substantive part of the host's immune response is directed. HVR1 is, however, hypervariable, and evades constantly the host's immune system. In contrast to suggestions by Farci et al., a successful vaccination strategy might be to direct the host's immune response towards a more constant region of HCV, which structure is more critical to HCV. In critical regions mutations might be less well tolerated by HCV.

Indeed, vaccination of chronically infected chimpanzees with HCV E1 protein clearly ameliorates the clinical outcome of an HCV infection, even in different subtypes (see, e.g. several abstracts by Maertens et al.; 943, AASLD Abstracts, Hepatology Vol. 28, No. 4 Pt 2, October 1998; Oral 8.6, 6th Int. Symp. on Hepatitis C & Related Viruses, NIH, June 6-9, 1999, copies attached). In this respect it is noteworthy that part of the chimpanzee's immune response was a cellular immune response. In addition, Rehmann et al. (1109, 406A, AASLD Abstracts, Hepatology October 1998, copy attached) suggest that CTL and Th response do play a role in viral clearance in human hosts, which can be maintained over a prolonged period of time after

infection. In Diepolder et al. (1997, J. Virology, 71: 6011-6019, copy attached) an immunodominant CD4⁺ T-cell epitope was identified in patients with self-limited acute hepatitis C infection.

Hence, humoral as well as cellular immune responses seem to be involved in a beneficial clinical outcome of an HCV infection, and thus in successful vaccination.

The presence of antibodies to most HCV proteins with chronic hepatitis C suggests that the humoral immune response to the virus is unable to stop the progression of disease. It is furthermore demonstrated that T cell epitopes have a positive effect in vaccination (see above and Botarelli et al. 1993, Gastroenterology 104: 580-587, copy attached).

As shown above, Farci's presuppositions are not correct, since there is success in the art and there are working examples.

It is, therefore, respectfully submitted that claims are supported by an enabling disclosure and withdrawal of the Section 112, first paragraph rejection is requested.

The Section 103 rejection of claims 49-51, 53 and 55-56 over Bukh (U.S. Patent No. 5,871,962) is traversed. Reconsideration and withdrawal of the rejection is requested in view of the following distinguishing remarks.

Bukh specifically concerns the disclosure of 51 new nucleotide sequences of HCV E1, and deduced amino acid sequences. Only prophetic experiments have been performed in that the nucleotide sequences have not been translated into peptides (see, Example 2, columns 22-25). Thus, these peptides have never been disclosed. More importantly, and obviously, no vaccines have been or could have been made using these putative peptides.

Consequently, the mere suggestion that vaccines could be generated with these imaginary proteins is fundamentally different from actually demonstrating that vaccines have been made

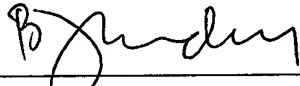
and the disclosure of Bukh provides no more than a wish to produce a product. Bukh provides therefore, at most, that it may have been obvious-to-try to make vaccines. "Obvious-to-try" however is not sufficient to establish a *prima facie* case of obviousness.

Therefore, it is respectfully submitted that the presently claimed invention is new and inventive over the Bukh disclosure. Withdrawal of the Section 103 rejection is requested.

In view of the above and attached, the claims are submitted to be in condition for allowance and a Notice to that effect is requested.

Respectfully submitted,

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Prevention of hepatitis C virus infection in chimpanzees by hyperimmune serum against the hypervariable region 1 of the envelope 2 protein

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ABSTRACT The identification of the neutralization domains of hepatitis C virus (HCV) is essential for the development of an effective vaccine. Here, we show that the hypervariable region 1 (HVR1) of the envelope 2 (E2) protein is a critical neutralization domain of HCV. Neutralization of HCV *in vitro* was attempted with a rabbit hyperimmune serum raised against a homologous synthetic peptide derived from the HVR1 of the E2 protein, and the residual infectivity was evaluated by inoculation of HCV-seronegative chimpanzees. The source of HCV was plasma obtained from a patient (H) during the acute phase of posttransfusion non-A, non-B hepatitis, which had been titrated for infectivity in chimpanzees. The anti-HVR1 antiserum induced protection against homologous HCV infection in chimpanzees, but not against the emergence of neutralization escape mutants that were found to be already present in the complex viral quasispecies of the inoculum. The finding that HVR1 can elicit protective immunity opens new perspectives for the development of effective preventive strategies. However, the identification of the most variable region of HCV as a critical neutralization domain poses a major challenge for the development of a broadly reactive vaccine against HCV.

Hepatitis C virus (HCV) is an important cause of morbidity and mortality worldwide (1-3). Infection with HCV becomes chronic in >80% of the cases and is a major cause of liver cirrhosis (4) and hepatocellular carcinoma (5). Although the development of a broadly reactive vaccine would be the most effective method for its control, concerns have been raised because of the high degree of genetic heterogeneity of HCV (6) and the lack of protective immunity against reinfection (7, 8) or superinfection (9, 10) documented both in humans and in chimpanzees. Viral isolate-restricted neutralizing antibodies against HCV have been demonstrated recently in infected individuals (11, 12), but their molecular target is presently unknown.

Several observations have suggested that the hypervariable region 1 (HVR1) could be involved in the neutralization of HCV. This assumption is based on the fact that the HVR1, which is located at the N terminus of the envelope glycoprotein 2 (E2) gene and consists of 34 amino acids spanning map position 384-414 (13), is the most variable region of the HCV genome (14, 15), contains linear epitopes that are recognized by patients' antibodies (16-22) and mutates rapidly *in vivo* (23-26), suggesting that it is under the selective pressure of the host immune system. This hypothesis is further substantiated by the lack of variability in the HVR1 observed in an agammaglobulinemic patient over a period of 2.5 years (27). Recent

data obtained *in vitro* suggest that antibodies, present in human sera and directed against the HVR1 as well as against the E2 protein of HCV, can prevent the binding of HCV to cells (28, 29). The potential importance of the HVR1 for HCV neutralization is also underscored by the analogy with the V3 loop of human immunodeficiency virus, which represents a principal neutralization domain and a major target of type-specific neutralizing antibodies (30).

To investigate whether the HVR1 of the E2 protein is a critical neutralization domain, *in vitro* neutralization of a pedigreed, *in vivo*-titrated HCV strain (H77) was attempted with a rabbit hyperimmune serum raised against a homologous synthetic HVR1 peptide. The residual infectivity was evaluated by inoculation of HCV-seronegative chimpanzees.

MATERIALS AND METHODS

Source of HCV. The virus stock of HCV used for all the inocula was derived from a plasmapheresis unit obtained during the early acute phase of posttransfusion non-A, non-B hepatitis (on July 12, 1977) from a patient (H) who underwent open heart surgery (31). This plasma, designated H77, contained 10^{6.5} 50% chimpanzee-infectious doses (CID₅₀) of HCV per ml, as shown by titration studies in chimpanzees (32) and was devoid of antibodies to HCV by all available tests. This viral stock has been used successfully to transmit non-A, non-B (NANB) hepatitis to chimpanzees in other studies (7, 14, 32).

Synthesis of the HVR1 Peptides and Generation of the Hyperimmune Sera. Two synthetic peptides (HVR1-A and HVR1-B; see Fig. 1) of 21 and 31 amino acids, respectively, corresponding to the sequence of the HVR1 of H77 were generated. The two sequences were obtained independently in our laboratory by direct sequencing, following PCR amplification of cDNA from the same sample (H77). One of the two sequences was previously reported (23). Peptides HVR1-A and HVR1-B were conjugated to tetanus antitoxin either by glutaraldehyde (HVR1-A) or by carbodiimide (HVR1-B) coupling. Hyperimmune sera were generated by three sequential intradermal multiple site injections in rabbits of the peptide conjugate (500 µg) in Freund's adjuvant according to a standard immunization protocol for rabbits (0, 1, and 6 months). The hyperimmune sera, designated LMF87 (anti-HVR1-A) and LMF92 (anti-HVR1-B), respectively, were

Abbreviations: HCV, hepatitis C virus; HVR1, hypervariable region 1; E1, envelope glycoprotein 1; E2, envelope glycoprotein 2; CID₅₀, 50% chimpanzee-infectious dose; NANB, non-A, non-B; ALT, alanine aminotransferase.

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tested in ELISA both against the homologous peptide (unconjugated) and against the recombinant E1/E2 complex from the H77 isolate expressed in vaccinia virus in BHK21 cells. The recombinant clone expressed in vaccinia had an HVR1 sequence identical to that of the HVR1-B peptide. As a control, the hyperimmune sera were tested against cell extracts of BHK21 infected with negative control recombinant vaccinia virus.

Source of Antibodies for Neutralization. As a potential source of neutralizing antibodies, we used the hyperimmune rabbit serum (LMF87, anti-HVR1) which was positive by ELISA against the homologous peptide and the recombinant E1/E2 protein complex, expressed in vaccinia systems. As negative controls, we used the preimmune rabbit serum that was negative by ELISA for all detectable antibodies to HCV, and plasma from a normal blood donor, negative for all antibodies to HCV (11), whose blood repeatedly failed to transmit hepatitis after transfusion (H.J.A., unpublished data). As a positive control, we used plasma obtained from patient H 2 years after primary infection, designated H79, which was previously shown to contain neutralizing antibodies against H77 (11). The H79 plasma was positive for antibodies to core, E2, NS3, NS4, and NS5 of HCV (11).

***In Vitro* Neutralization Test.** The neutralization test was performed as described (11). Each antiserum was diluted 1:5 in PBS (pH 7.4) and then heat-inactivated at 56°C for 30 min before use. One vial of a dilution (in fetal bovine serum) of the challenge virus containing 3200 CID_{50} was further diluted 1:5 in ice-cold PBS (pH 7.4), and then one additional dilution was made in cold PBS with 20% fetal bovine serum to yield samples containing 64 CID_{50} . The *in vitro* neutralization test was done by mixing the virus inoculum (64 CID_{50} in 1 ml) with one of the inactivated antisera (1 ml). The virus/antiserum mixtures were incubated overnight at 4°C. Each mixture (2 ml) was then inoculated intravenously into one HCV-seronegative chimpanzee.

Chimpanzees. Five chimpanzees were included in this study. The animals were caged individually and maintained under conditions that met all relevant requirements for the use of primates in an approved facility. None of the chimpanzees included in this study had been previously exposed to HCV, and none of them had signs of active or past HCV infection, as measured by PCR and antibody testing. At the time of the study, all chimpanzees were negative for hepatitis B surface antigen and had normal hepatic enzyme levels. Weekly serum samples were monitored for alanine aminotransferase (ALT). Serum HCV RNA was determined in serial serum samples obtained at intervals of 1, 2, or 4 weeks, during an observation period of 24 weeks after the virus challenge. All serial samples were tested with a set of nested primers derived from the 5' noncoding region of the HCV genome (7). Serum HCV RNA from selected samples obtained from each chimpanzee 2 weeks after inoculation was amplified with a set of primers that span part of the E1 and E2 genes (7), including the HVR1, and the PCR products were sequenced both directly and after molecular cloning. Weekly serum samples were also tested for antibodies to HCV (anti-HCV).

Anti-HCV Testing. Antibodies against structural and non-structural proteins of HCV (anti-HCV) were assayed in chimpanzee sera using a second generation ELISA according to the manufacturer's instructions (Ortho Diagnostics).

RNA Extraction and PCR. Total RNA extracted from 100 μl of serum or plasma using the guanidinium/phenol/chloroform method (33) was reverse-transcribed in a volume of 20 μl , and the resulting cDNA was amplified in a 100- μl reaction volume (33). PCR was performed using two sets of nested primers (7). The first, derived from the 5' noncoding region (7), was used to investigate the course of HCV viremia, and the second, derived from the E1 and E2 genes (7), including the HVR1, for the comparative sequence analysis.

The sensitivity, specificity, and details of our nested PCR technique, have been reported (7, 33). To reduce the risk of contamination, all the proper precautions were taken (7, 33). In addition, for each test sample, a negative control was tested in parallel throughout the entire procedure, starting from RNA extraction.

Sequencing Analysis. PCR products amplified with the set of primers that span part of the E1 and E2 genes of the HCV genome, obtained from the H77 inoculum and from a selected sample from each chimpanzee, were purified by GeneClean (Bio 101). Double-stranded PCR fragments were directly sequenced by the dideoxynucleotide chain termination method with phage T7 DNA polymerase (Sequenase; United States Biochemical), as described (34). The amplified PCR products were also cloned into pGEM-T vector systems (Promega), and the molecular clones were sequenced using the Applied Biosystems model 373 automated DNA sequencer with a modified Sanger method. A total of 104 molecular clones from the H77 inoculum and 9 or 10 clones from each chimpanzee, on a sample obtained 2 weeks after inoculation, were sequenced.

RESULTS

Generation of Rabbit Hyperimmune Sera Against the HVR1 and *In Vitro* Neutralization. We generated rabbit hyperimmune sera directed against two synthetic peptides corresponding to the HVR1 of HCV, strain H77, a pedigreed virus obtained during the early acute phase of post-transfusion NANB hepatitis from a patient (H) who underwent open heart surgery (31). Two separate aliquots of the H77 plasma were PCR-amplified with a set of primers spanning a portion of the E1 and E2 genes (7), including the HVR1 domain, and the DNA products were analyzed by direct sequencing (Fig. 1). Comparative analysis of the two predicted amino acid sequences of 191 residues showed only a single amino acid change (S \rightarrow N at position 391), located within the HVR1 (Fig.

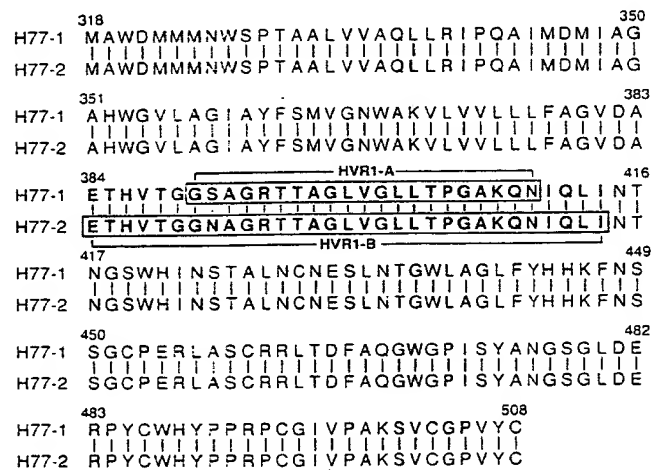


FIG. 1. Alignment of the amino acid sequences (in single-letter code) predicted from a portion of the E1 and E2 genes of HCV, strain H77, spanning map positions 317-508 (13). H77 denotes the sample obtained from a plasmapheresis unit collected from patient H during the acute phase of posttransfusion NANB hepatitis (31), which represents the standard viral stock used for all the inocula, which had been previously titrated in chimpanzees (32). H77-1 and H77-2 denote two distinct sequences obtained independently in our laboratory by direct sequencing, following PCR amplification of cDNA from the same sample (H77). One of the two sequences was previously reported (23). The HVR1 of the E2 protein, spanning map position 384-414 (13), is shown in boldface type. The boxed sequences denote the sequence of the peptides (HVR1-A and HVR1-B) used for generating hyperimmune rabbit sera. Matches are indicated by vertical bars and changes are indicated by colons.

Table 1. *In vitro* neutralization of HCV, as measured in chimpanzees: animals and antisera used

Chimpanzee no.	Sera reacted with 64 CID ₅₀ of HCV, strain H77 and inoculated into indicated chimpanzee	
	Serum (final concentration)	Anti-HCV antibodies* detected in indicated serum
1480	Preimmune rabbit serum (1:10)	None
1479	Normal human plasma (1:10)	None
1484, 1486	Hyperimmune rabbit anti-HVR1 (1:10)	Homologous HVR1 peptide, recombinant E1/E2 complex
1475, 1442	H79 human plasma (1:10)	Core, E1, E2, NS3, NS4, NS5

*Anti-HCV antibodies directed against HVR1 (synthetic peptide with sequence of hypervariable region 1), NS3 (nonstructural 3 protein), NS4 (nonstructural 4 protein), NS5 (nonstructural 5 protein, detected by ELISA).

1). Based on these data, two synthetic peptides, representing the two sequences of the HVR1 of H77, were generated, and each of them was separately used to immunize two rabbits. One peptide (HVR1-A), bearing the S residue at position 391, was shorter (aa 390–410); the other (HVR1-B), bearing the N residue at position 391, was longer (aa 384–414). The hyperimmune sera, designated LMF87 (anti-HVR1-A) and LMF92 (anti-HVR1-B), respectively, were both reactive in an ELISA test against the homologous peptide (at a titer of 1:650,000), but only LMF87, directed against the shorter peptide (HVR1-A), recognized the recombinant E1/E2 protein complex derived from the H77 virus and expressed in a vaccinia system (at a titer of 1:70,000). Thus, the LMF87 anti-HVR1 serum was selected for *in vitro* neutralization experiments.

The chimpanzees and sera used in the experiments of HCV neutralization *in vitro* are indicated in Table 1. As negative controls, we used the respective preimmune rabbit serum and

plasma from a normal blood donor, which were both negative for detectable antibodies to HCV. As a positive control, we used plasma obtained from patient H 2 years after primary infection, designated H79, which was previously shown to contain neutralizing antibodies against H77 (11). The protocol used for the neutralization test has been reported (11). The challenge stock was prepared from the standard H77 inoculum which contained 10^{6.5} CID₅₀ of HCV per milliliter, as determined by *in vivo* titration in chimpanzees (32). This inoculum had been used successfully for other challenge studies in chimpanzees (7, 11, 32). The *in vitro* neutralization test was performed by mixing the virus inoculum (64 CID₅₀ in 1 ml) with the relevant serum (1 ml), previously heat-inactivated at 56°C for 30 min. The virus/serum mixtures were incubated overnight at 4°C and then inoculated i.v. into seronegative chimpanzees (Table 1). The dose of H77 virus used in this study (64 CID₅₀) had successfully infected five of five chimpanzees in a previous study (11).

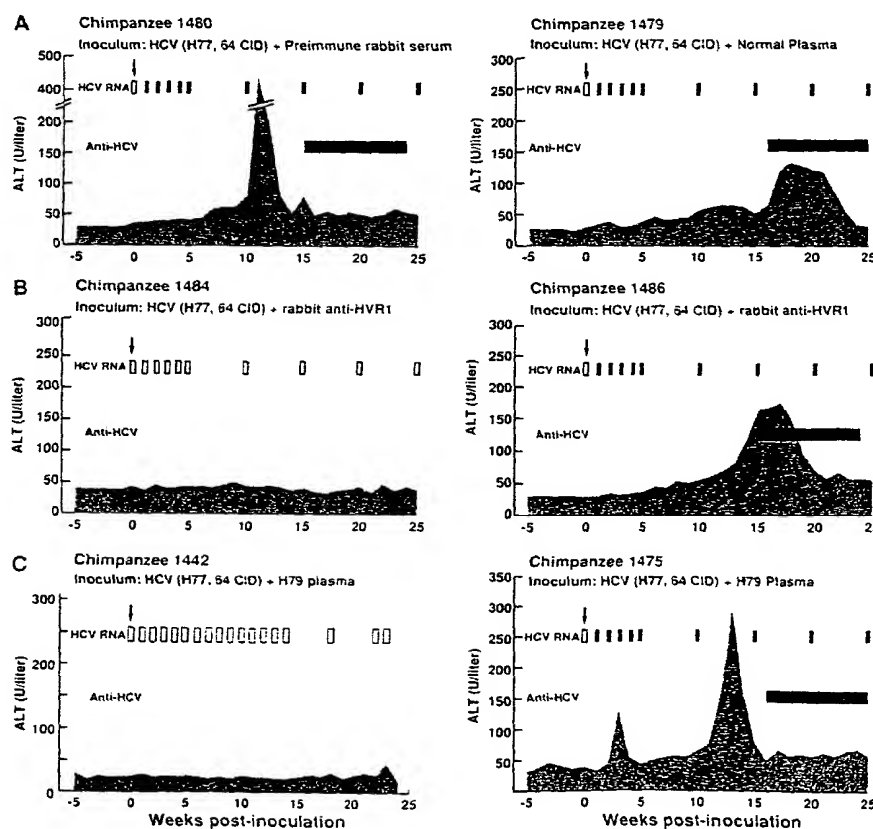


FIG. 2. Course of HCV infection in chimpanzees after antibody-mediated *in vitro* neutralization. Details of the *in vitro* neutralization test, of the source of HCV, and of the antisera used in this study are provided in *Materials and Methods*. Neutralization of HCV was attempted with the preimmune rabbit serum and with an anti-HCV negative human plasma (A), with the hyperimmune rabbit anti-HVR1 serum (B), or with the H79 human plasma (C). The upper arrows indicate the time of challenge. The shaded areas indicate the values of serum ALT. Normal ALT values in chimpanzees range between 6 and 38 units/liter. Open bars indicate negative results for serum HCV RNA by PCR and solid bars indicate positive results. The horizontal bar indicates the time during which serum was positive for antibodies to HCV, as detected by second generation ELISA assay. Chimpanzee 1442 was described previously (11).

Sequence Analysis of the H77 Virus Used for Inoculation. To interpret the results of the neutralization experiments, we performed an extensive sequence analysis of the H77 virus that was used for inoculation. RNA from the H77 viral stock was extracted, reverse transcribed, and amplified with a set of primers that span a portion of the E1/E2 region, including the HVR1 (7). The PCR products, 573 nt long, were purified and analyzed by both direct sequencing and sequencing of molecular clones. From the H77 viral stock, a total of 104 molecular clones was analyzed. The predicted amino acid sequences of

Comparative Sequence Analysis of the Viral Quasispecies Present in the H77 Inoculum and the Viruses Recovered from the Infected Chimpanzees. We performed a comparative sequence analysis of the viral strains present in the H77 inoculum and the viruses recovered from the chimpanzees that developed HCV infection after challenge. From each chimpanzee, both direct sequencing and sequencing of 9 or 10 molecular clones were performed on a sample obtained 2 weeks after inoculation (Fig. 4). Remarkably, in the animal whose inoculum contained the virus mixed with the hyperimmune rabbit anti-HVR1 serum (no. 1486), neither the sequence of the 10 molecular clones nor the direct sequence was identical to the predominant clone against which the hyperimmune serum was directed. The viruses emerging from this animal were identical to two of the minor variants: 7 of the 10 clones corresponded to the second variant (6%) in the H77 quasispecies; the remaining 3 clones, as well as the directly determined sequence, corresponded to a variant represented by only 2% of the H77 quasispecies (Figs. 3 and 4). When compared with the sequence of the predominant strain of H77 virus used for challenge (Figs. 3 and 4), each of the two minor variants exhibited 4 amino acid changes over the 31 amino acids of the HVR1. In contrast, viruses identical to the predominant clone were consistently recovered from all the other chimpanzees, regardless of the serum used for neutralization. Altogether, these data indicate that in animal no. 1486 the rabbit hyperimmune anti-HVR1 serum was able to neutralize the predominant clone against which it had been raised.

384										414									
H77 ETHVTGG										S _N AGRTTAGLVGLLTPGAKQNIQLI									
No. of Clones																			
70	N
6	S	.	.	.	I	.	.	FT	.	.	.
5	S	.	H
4	N	S	.	.	.
2	N	.	.	.	A
2	AS	S	.	.	.
2	S	.	H	R	.	S	.
2	S	.	H	.	A	.	IA	.	F	.	L
1	N	C	.	.	.
1	N	D	.	.	.
1	NT
1	N	H	.	.	.
1	N	P	.	.	.
1	N	A
1	.	.	R	N	S	.	.	.
1	S	.	.	.	I	.	.	T	.	.	.
1	S	.	H	.	.	.	P	R	.	S	.
1	R	.	.	.	S	.	.	.	I	.	FT
1	.	.	.	R	.	S	.	.	S	.	H	.	A	.	IA	.	F	.	L

FIG. 3. Predicted amino acid sequence alignment of 31 amino acids (in single-letter code) representing HVR1 of the E2 gene, spanning map position 384-414, of 104 molecular clones obtained from HCV, strain H77, which was used for inoculation. The sequence obtained by direct sequencing is indicated at the top for comparison. The standard viral stock used for all the inocula (H77) was obtained from patient H during the acute phase of posttransfusion NANB hepatitis (31). The remaining sequence of the 191 amino acids spanning map position 318-508, which is not shown, is available upon request.

Chimpanzee No.	Inoculum		384																										414									
			H77	E	T	H	V	T	G	G	S	N	A	G	R	T	A	G	L	V	G	L	L	T	P	G	A	K	Q	N	I	Q	L	I				
1486	HCV (H77, 64 CID) + Rabbit anti-HVR1	7 clones	S	I	.	.	F	T		
		3 clones	S	.	.	H	R	.	S			
		Dir. seq.	S	.	.	H	R	.	S		
1480	HCV (H77, 64 CID) + Preimmune rabbit serum	5 clones	S	I	.	.	F	T			
		3 clones	N		
		1 clone	S	I	.	V	.	F	T			
		Dir. seq.	S	I	.	F	T			
1479	HCV (H77, 64 CID) + Normal Plasma	8 clones	S	I	.	.	F	T			
		2 clones	N		
		Dir. seq.	S	I	.	F	T			
1475	HCV (H77, 64 CID) + H79 Plasma	7 clones	N			
		2 clones	N	S			
		Dir. seq.	N		

FIG. 4. Comparative sequence analysis of the sequence of the H77 virus used for inoculation and the viruses recovered from the chimpanzees 2 weeks after inoculation. The two sequences indicated for H77 were obtained independently by direct sequencing (Dir. seq.). For each chimpanzee the results of both direct sequencing and sequencing of 9 or 10 molecular clones are indicated.

but was ineffective against some of the minor variants that emerged *in vivo*. Comparative sequence analysis was also performed in animal no. 1475, which developed acute hepatitis despite the presence in the inoculum of the H79 plasma, previously shown to contain neutralizing antibodies (11). The analysis demonstrated that the virus emerging *in vivo* was identical to the predominant clone (67% of the H77 viral quasispecies). Only a single amino acid change was detected in two of the nine clones. Similarly, the sequence obtained by direct sequencing corresponded to that of the predominant clone. Because this animal exhibited a biphasic pattern of serum ALT levels (Fig. 2C), raising the possibility that the second peak of hepatitis might be due to the emergence of a neutralization escape mutant, additional direct sequence analysis was performed over a period of 6 months after inoculation. Comparison of the sequences obtained 8, 12, 13, 18, and 25 weeks, respectively, postinoculation demonstrated 100% identity with the direct sequence obtained at week 2 postinoculation (Fig. 4). Remarkably, none of the minor variants was ever detected in this chimpanzee, which suggests that the *in vitro* neutralization was incomplete, and that HCV infection in this animal was initiated by a very limited number of viral particles of the predominant strain that were not effectively neutralized. These data support the hypothesis that the neutralizing immune response elicited by HCV in the host is weak, and further demonstrate the extreme sensitivity of the animal model for evaluating HCV infectivity (35).

DISCUSSION

Our study provides evidence that the HVR1 of the E2 protein of HCV, the most variable region of the entire viral genome, is a critical neutralization domain. We showed that a hyperimmune rabbit serum raised against a synthetic peptide representing the HVR1 protected chimpanzees from homologous HCV infection, but not from the emergence of neutralization escape mutants that were already present in the complex viral quasispecies. These results indicate that the synthetic peptide had elicited neutralizing antibodies, but that such antibodies were type-specific and thus ineffective against some of the minor variants present in the inoculum. In fact, the rabbit anti-HVR1 hyperimmune serum was directed against the predominant clone present in the H77 plasma, which contained a mixed viral population (quasispecies) of at least 19 different variants. Thus, this study provides an *in vivo* model for the emergence of neutralization escape mutants, a strategy whereby HCV can evade the host's immune surveillance and establish persistent infection in >80% of infected individuals (4). Neutralization escape mutants emerged in only one of the

two animals whose inoculum contained the virus mixed with the hyperimmune anti-HVR1 serum, whereas the other chimpanzee was completely protected. A possible explanation for this finding is the different infectivity titer of each of the 19 viral variants present in the H77 inoculum. In fact, the two variants recovered from this animal represented only 6% and 2%, respectively, of the viral population of the H77 used for inoculation. Thus, the viral inoculum of 64 CID₅₀ contained only ≈4 and 1 CID₅₀, respectively, of these variants. These represent borderline titers for *in vivo* infectivity, which would not be expected to infect 100% of the animals, based on Poisson distributions of the variant viruses.

The observation that a hyperimmune serum against the HVR1 protected chimpanzees from homologous HCV infection provides direct evidence that anti-HVR1 antibodies can, in the absence of other virus-specific immune responses, prevent HCV infection. The HCV-neutralizing activity mediated by anti-HVR1 antibodies may be the experimental correlate of an *in vivo* protective immune response. Protection against the homologous strain of HCV was demonstrated in chimpanzees vaccinated with the recombinant putative E1/E2 proteins of HCV (36). The finding that HVR1 is a neutralization domain of HCV constitutes an important step for understanding the immune response elicited by HCV in the host, as well as for devising effective preventive strategies for the control of HCV infection. However, the fact that a major target of the neutralizing antibodies is the HVR1, the most variable region of the HCV genome, raises a new set of problems that need to be addressed for the development of a broadly reactive vaccine against HCV. For a vaccine to be practical in humans, it should provide protection against the great variety of HCV isolates that infect the human population. The high degree of genetic heterogeneity of HCV (6), which is reflected in the complex quasispecies nature of this virus (37), indicates that it might be difficult to realize effective preventive strategies. Nevertheless, our report demonstrates that it is indeed possible to elicit a protective humoral immune response against homologous HCV infection. However, because there is no obvious strategy to suppress the genetic variation of HCV, the finding that the HVR1 is a neutralization domain poses a major challenge that must be taken into account for any viable vaccination strategy for the control of HCV infection.

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